REMARKS

This application has been amended in a manner that is believed to place it in condition for allowance at the time of the next Official Action.

Claims 22-24, 30-34 and 39-40 are pending in the present application. Claims 22-24, 30-34 and 39-40 have been amended to address the formal matters raised in the pending Office Action and Advisory Action. Claims 25-29 and 35-38 have been cancelled.

Claims 22-38 were rejected under 35 USC §101 as allegedly being directed to non-statutory subject matter. Applicants believe that the present amendment obviates this rejection.

In imposing the rejection, the Official Action alleged that the claimed method did not provide an immediate, concrete, tangible, and useful result. However, applicants believe that the claimed invention satisfies the requirements of 35 USC §101.

In particular, the Examiner's attention is respectfully directed to independent claim 22. Claim 22 recites a step "... to locate a gene associated with a certain phenotype...". The basis for this amendment can be found in the specification at page 7, lines 8 (step (iii)). The specification provides that the present method results in locating a gene of interest, is the object of the gene mapping process. As a result, applicants believe that the present amendment obviates this rejection.

Claims 22-40 were rejected under 35 USC 112 as being indefinite. Applicants believe that the present amendment obviates this rejection.

Claims 22-24, 30-34 and 39-40 have been drafted in a manner to address the formal matters raised in the pending Office Action. In particular, claim 22 has been amended to recite a method for gene mapping to locate a gene associated with a certain phenotype from a dataset of chromosome and phenotype data by analyzing an association between phenotype and genetic markers m_i.

The data or dataset from which the gene of interest is sought after is derived from the chromosome and phenotype data. The input to the method is a dataset wherein each record describes an individual (or, alternatively, each record describes a single chromosome). Each record is comprised of alleles of genetic markers, of a value of the phenotype under study, and of zero or more of the following: values of individual covariates, values of environmental variables, and values of auxiliary phenotypes.

The input dataset may be obtained in a medical study using different techniques, such as wet lab experiments. This data may already exist and it can be obtained for example by the GENEHUNTER program as mentioned on page 5 of the present specification.

On the third line of claim 22, an informality was present in that the word "marks" should have been "markers". Moreover, in step i) b: there should be "pattern evaluation function" instead of "pattern evaluation". These matters have been corrected.

In step i) there are two amendments referring to "said" data "set", just to more particularly point out and distinctly claim the present invention.

In step i) "b:" the pattern evaluation function has been clarified to recite that "true if and only if there is a strong association between the marker pattern *P* and a phenotype being studied", as mentioned in the present specification at page 5, line 12. As it can be seen in the algorithms presented the pattern evaluation function is a value function.

In step iii) the indefinite term "evaluating" has been removed and the wording of the claim has been amended to set forth a positive active method step. The gene can be located to a marker or to a chromosomal region containing a set of markers, as mentioned for example on page 5, lines 10-11 in the present specification.

While the Office Action does not find the sentence "a: the marker patterns are expressions within said database ..." in step i) clear, a marker pattern is a *logical* expression about markers and alleles (and potentially about values of individual covariates, values of environmental variables, and values of

auxiliary prototypes) of the data set, so that the pattern can be tested on any single record in the data set, and the rest results either in "true" (meaning that the pattern matches the record) or "false" (the pattern does not match the record). The pattern evaluation function *e(P)* is true if and only if the association between the marker pattern *P* and the phenotype being studied is strong, wherein association strength is defined by the different between the distributions of the phenotype values among those records that match and those records that do not match the pattern.

Claim 30 has been amended to contain a definition for the sign of X^2 "... wherein said signed value of the X^2 is negative if the relative frequency of the haplotype pattern among the control chromosomes is higher than that of the trait-associated chromosomes, and otherwise positive" (page 15, lines 15-18).

As noted above, claims 25-29 and 35-38 have been cancelled.

In view of the above, applicants believe that the claimed invention is definite to one skilled in the art.

In view of the present amendment and the foregoing Remarks, therefore, applicants believe that the present application is in condition for allowance at the time of the next Official Action.

The Commissioner is hereby authorized in this, concurrent, and future replies, to charge payment or credit any overpayment to Deposit Account No. 25-0120 for any additional fees required under 37 C.F.R. § 1.16 or under 37 C.F.R. § 1.17.

Respectfully submitted,

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